PCT/US99/25/39

### 1/23

#### **BAL human cDNA**

5'UTR:

GGGCTTCGTGTTCCTGGGTGCTGACCGTGCACTCCCCGCCGCCGCGAGGACTTAGAGCTCTGGAAGT AGCTCTCCAGCTTCCTTCGTACTCGGGGGCCGGACTTGTACACCCGCACGAGGAGCGGGACGGC GGGCGCAGAAGTGGGCCACCATATCTGGAAACTACAGTCTATGCTTTGAAGCGCAAAAGGGAATA AACATTTAAAGACTCCCCCGGGGACCTGGAGG

Coding: alternatively spliced sequence in bold characters

1 1

ATGGACTTTTCCATGGTGGCCGGAGEAGCAGCTTACAATGAAAAATCAG**GTAGGATTACCTCGCT** CTCACTCTTGTTTCAGAAAGTCTTTGCTCAGATCTTTCCTCAGTGGAGAAAGGGGAATACAG **AAGAATGTCTCCCCTACAAGTGCTCAG**AGACTGGTGCTCTTGGAGAAAACTATAGTTGGCAAAT TCCCATTAACCACAATGACTTCAAAATTTTAAAAAATAATGAGCGTCAGCTGTGTGAAGTCCTCCA GAATAAGTTTGGCTGTATCTCTACCCTGGTCTCTCCAGTTCAGGAAGGCAACAGCAAATCTCTGCA AGTGTTCAGAAAAATGCTGACTCCTAGGATAGAGTTATCAGTCTGGAAAGATGACCTCACCACAC ATGCTGTTGATGCTGTGGAATGCAGCCAATGAAGATCTTCTGCATGGGGGAGGCCTGGCCCTGG CCCTGGTAAAAGCTGGTGGATTTGAAATCCAAGAAGAGAGCAAACAGTTTGTTGCCAGATATGGT AAAGTGTCAGCTGGTGAGATAGCTGTCACGGGAGCAGGGGAGGCTTCCCTGCAAACAGATCATCCA TGCTGTTGGGCCTCGGTGGATGGAATGGGATAAACAGGGATGTACTGGAAAGCTGCAGAGGGCCA TTGTAAGTATTCTGAATTATGTCATCTATAAAAATACTCACATTAAGACAGTAGCAATTCCAGCCT TGAGCTCTGGGATTTTTCAGTTCCCTCTGAATTTGTGTACAAAGACTATTGTAGAGACTATCCGGGT CTACTGTTGCTGCCTTTAAAGCTGCTTCAGAATTCATCCTAGGGAAGAGTGAGCTGGGACAAGAAA CCACCCTTCTTTCAATGCAATGGTCGTGAACAACCTGACCCTCCAGATTGTCCAGGGCCACATTG AATGGCAGACGGCAGATGTAATTGTTAATTCTGTAAACCCACATGATATTACAGTTGGACCTGTGG CATGTACTGTGGCATTCAGAATTTCCTAAACCTCAGATATTAAAACATGCAATGAAGGAGTGTTTG GAAAAATGCATTGAGCAAAATATAACTTCCATTTCCTTTCCTGCCCTTGGGACTGGAAACATGGAA ATAAAGAAGGAAACAGCAGCAGAGATTTTGTTTGATGAAGTTTTAACATTTGCCAAAGACCATGT AAAACACCAGTTAACTGTAAAATTTGTGATCTTTCCAACAGATTTGGAGATATATAAGGCTTTCAG TTCTGAAATGGCAAAGAGGTCCAAGATGCTGAGTTTGAACAATTACAGTGTCCCCCAGTCAACCA GAGAGGAGAAAAGAGAAAATGGGCTTGAAGCTAGATCTCCTGCCATCAATCTGATGGGATTCAAC GTGGAAGAGTGTAGTGAGGCCCACGCATGGATCCAAAGAATCCTGAGTCTCCAGAACCACCACA TCATTGAGAATAATCATATTCTGTACCTTGGGAGAAAGGAACATGACATTTTGTCTCAGCTTCAGA GCCCGGGCTGACCTCATTGAGGTGGTTATGAACATTGAAGATATGCTTTGTAAAGTACAGGAGGA AATGGCAAGGAAAAAGGAGCGAGGCCTTTGGCGCTCGTTAGGACAGTGGACTATTCAGCAACAAA AAACCCAAGACGAAATGAAAGAAAATATCATATTTCTGAAATGTCCTGTGCCTCCAACTCAAGAG CTTCTAGATCAAAAGAAACAGTTTGAAAAATGTGGTTTGCAGGTTCTAAAGGTGGAGAAGATAGA CAATGAGGTCCTTATGGCTGCCTTTCAAAGAAAGAAAAAATGATGGAAGAAAAACTGCACAGGC AACCTGTGAGCCATAGGCTGTTTCAGCAAGTCCCATACCAGTTCTGCAATGTGGTATGCAGAGTTG GCTTTCAAAGAATGTACTCGACACCTTGCGATCCAAAATACGGAGCTGGCATATACTTCACCAAGA ACCTCAAAAACCTGGCAGAGAAGGCCAAGAAAATCTCTGCTGCAGATAAGCTGATCTATGTGTTT GAGGCTGAAGTACTCACAGGCTTCTTCTGCCAGGGACATCCGTTAAATATTGTTCCCCCACCACTG AGTCCTGGAGCTATAGATGGTCATGACAGTGTGGTTGACAATGTCTCCAGCCCTGAAACCTTTGTT ATTTTTAGTGGCATGCAGGCTATACCTCAGTATTTGTGGACATGCACCCAGGAATATGTACAGTCA CAAGATTACTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGG CAGCCCTGTTGATTAA

Fig. 1



BAL human protein: alternatively spliced (Bold characters)

MDFSMVAGAAAYNEKSGRITSLSLLFQKVFAQIFPQWRKGNTEECLPYKCSETGALGENYSW
QIPINHNDFKILKNNERQLCEVLQNKFGCISTLVSPVQEGNSKSLQVFRKMLTPRIELSVWKDDLTT
HAVDAVVNAANEDLLHGGGLALALVKAGGFEIQEESKQFVARYGKVSAGEIAVTGAGRLPCKQIIHAV
GPRWMEWDKQGCTGKLQRAIVSILNYVIYKNTHIKTVAIPALSSGIFQFPLNLCTKTIVETIRVSLQGKP
MMSNLKEIHLVSNEDPTVAAFKAASEFILGKSELGQETTPSFNAMVVNNLTLQIVQGHIEWQTADVIVN
SVNPHDITVGPVAKSILQQAGVEMKSEFLATKAKQFQRSQLVLVTKGFNLFCKYIYHVLWHSEFPKPQI
LKHAMKECLEKCIEQNITSISFPALGTGNMEIKKETAAEILFDEVLTFAKD
HVKHQLTVKFVIFPTDLEIYKAFSSEMAKRSKMLSLNNYSVPQSTREEKRENGLEARSPAINLMGFNVE
EMYEAHAWIQRILSLQNHHIIENNHILYLGRKEHDILSQLQKTSSVSITEIISPGRTELEIEGARADLIEVV
MNIEDMLCKVQEEMARKKERGLWRSLGQWTIQQQKTQDEMKENIIFLKCPVPPTQELLDQKKQFEKC
GLQVLKVEKIDNEVLMAAFQRKKKMMEEKLHRQPVSHRLFQQVPYQFCNVVCRVGFQRMYSTPCDP
KYGAGIYFTKNLKNLAEKAKKISAADKLIYVFEAEVLTGFFCQGHPLNIVPPPLSPGAIDGHDSVVDNVS
SPETFVIFSGMQAIPQYLWTCTQEYVQSQDYSSGPMRPFAQHPWRGFASGSPVD

Fig. 1 (continued)

#### BAL mouse cDNA:

5'UTR

AGGAACGGAAGTTTGGCGGGAACCCGGATTCCCAGGTTCAGGCCTCTCAAGGGTGGAGCGGAATA ATCTGAAGACCCACGTGGGACCTGAAGAATGGCCTATTAC

Coding region (shorter form only)

ATGGATACATGGGCGGCAGCTCCCGCCGAAAGACCCAGCCAACAATTCTCTTGAAGAACATTATAG ATGGCAAATTCCCATTAAACACAATGTCTTCGAAATTTTAAAGAGCAATGAGAGTCAGCTATGTGA AGTCCTCCAAAATAAGTTTGGATGCATCTCTACCCTGAGCTGTCCAACTCTAGCAGGGAGCAGCTC CCTTACCAGACACGTTGTTGATGCTGTGGTGAACGCAGCCAATGAAAACCTTTTTGCATGGAAGTGG CCTGGCCGGAAGCTTGGTGAAAACTGGTGGCTTTGAAATCCAAGAAGAGAGCAAAAGAATCATTG  ${\tt CCAACGTTGGTAAAATCTCAGTTGGTGGAATCGCTATCACCGGTGCGGGGAGACTTCCTTGCCATT}$ TGATTATCCATGCGGTTGGACCTCGGTGGACAGTTACGAACAGCCAGACAGCTATCGAATTACTGA AATTTGCCATTAGGAACATTCTAGATTATGTCACCAAATATGATCTACGCATTAAGACAGTAGCAA TTCCAGCCCTGAGCTCTGGAATTTTCCAGTTCCCTCTGGATTTGTGTACAAGCATAATTTTAGAAAC TTGGGGGGGTCCAGAAACTGACCCTGCTTCCACCATGACTCTTCGCATCGGCCGGGGCCTGACTCT CCAGATTGTCCAAGGCTGTATTGAAATGCAAACAACAGATGTAATTGGTAATTCTGGATACATGCA GGATTTTAAATCAGGACGAGTGGCACAGTCGATTCTTAGACAAGCAGGGGTTGAAATGGAAAAGG AACTTGACAAGGTTAACCTGTCCACAGATTATCAAGAGGTGTGGGTCACAAAAGGATTTAAATTGT CCTGTCAGTATGTCTTCCATGTGGCATGGCATTCCCAAATCAACAAATACCAGATATTGAAAGATG CAATGAAGTCCTGTCTAGAAAAATGCCTTAAACCAGATATAAATTCCATTTCCTTTCCTGCTCTCG GGACAGGATTGATGGATTTGAAGAAGAGTACAGCAGCTCAGATAATGTTTGAGGAAGTTTTTTGCA TTTGCTAAAGAGCACAAGGAAAAAACGCTAACTGTAAAGATTGTGATCTTTCCAGTAGATGTGGA GACGTACAAGATTTTTTATGCTGAAATGACAAAAAGGTCCAACGAGCTGAATCTCAGCGGTAATA GTGGTGCTTTAGCCCTGCAGTGGTCCAGTGGGGAGCAAAGAAGAGGCGGCCTTGAAGCTGGATCT CCTGCCATCAATCTCATGGGTGTAAAAGTGGGAGAGATGTGTGAGGCCCAGGAATGGATTGAAAG GTTGCTGGTCTCCCTGGACCACCACATCATTGAGAATAATCATATTCTCTATCTTGGGAAAAAAAGA GCACGACGTGCTGTCTGAGCTCCAGACCAGCACAAGAGTCTCCATTTCAGAGACTGTCAGTCCAA GAACGGCCACTTTGGAGATTAAAGGTCCCCAGGCTGACCTCATTGACGCAGTTATGAGGATTGAAT GTATGCTGTGTGACGTTCAGGAAGAAGTGGCAGGAAAAAGGGAGAAAAATCTTTGGAGCTTGTCA GGACAGGGGACCAACCAGCAAGAAAAACTGGATAAAATGGAAGAATCGTACACATTTCAACGAT GTTGTGCAGGTGGAGCAGATAGACAATAAGGTGCTGCTGCCTTCCAAGAGAAGAAGAAAAT GATGGAAGAGGACGCCAAAGGGATCTGGGAGCCAAAGGTTGTTTCAGCAGGTCCCACATCAGT TCTGCAATACGGTGTGCAGAGTCGGCTTCCACAGAATGTATTCGACATCCTATAACCCAGTTTATG GAGCCGGCATATATTTCACCAAGAGCCTCAAAAATCTAGCAGACAAGGTCAAGAAAACCTCAAGC ACAGACAAGCTAATCTATGTGTTTGAGGCAGAAGTACTCACAGGGTCCTTCTGTCAGGGTAATTCC TCAAATATCATCCCTCCACCATTGAGTCCTGGGGCCTTAGATGTCAATGACAGCGTAGTTGACAAT  ${\tt GTTTCCAGCCCTGAAACCATTGTTGTTTTTAATGGCATGCAGGCCATGCCCCTGTACTTGTGGACTT}$ GCACACAGGATAGGACATTCTCACAGCATCCGATGTGGTCACAGGACTACTCATCAGGACCAGGA ATGGTCTCTTCGCTGCAGTCCTGGGAATGGGTCTTAAATGGCAGCTCTGTTTAG

3'UTR:

CCTGTTCAGAATGATGGGGTCACTAAAGGCACCGACCACACACTAGCATCATAGTGCCTTTGTCTT TACCTCTGGGCTTGACTGGGCAGATGCCAGCTAAAACTTCCTCACTGTCTT

Fig. 2



### BAL mouse protein (shorter form):

MDTWAAAPAERPANNSLEEHYRWQIPIKHNVFEILKSNESQLCEVLQNKFGCISTLSCPTLAGSSS
PAQRVFRRTLIPGIELSVWKDDLTRHVVDAVVNAANENLLHGSGLAGSLVKTGGFEIQEESKRIIA
NVGKISVGGIAITGAGRLPCHLIIHAVGPRWTVTNSQTAIELLKFAIRNILDYVTKYDLRIKTVAIPA
LSSGIFQFPLDLCTSIILETIRLYFQDKQMFGNLREIHLVSNEDPTVASFKSASESILGRDLSSWGGP
ETDPASTMTLRIGRGLTLQIVQGCIEMQTTDVIGNSGYMQDFKSGRVAQSILRQAGVEMEKELDK
VNLSTDYQEVWVTKGFKLSCQYVFHVAWHSQINKYQILKDAMKSCLEKCLKPDINSISFPALGT
GLMDLKKSTAAQIMFEEVFAFAKEHKEKTLTVKIVIFPVDVETYKIFYAEMTKRSNELNLSGNSG
ALALQWSSGEQRRGGLEAGSPAINLMGVKVGEMCEAQEWIERLLVSLDHHIIENNHILYLGKKE
HDVLSELQTSTRVSISETVSPRTATLEIKGPQADLIDAVMRIECMLCDVQEEVAGKREKNLWSLS
GQGTNQQEKLDKMEESYTFQRYPASLTQELQDRKKQFEKCGLWVVQVEQIDNKVLLAAFQE K
KKMMEERTPKGSGSQRLFQQVPHQFCNTVCRVGFHRMYSTSYNPVYGAGIYFTKSLKNLADKV
KKTSSTDKLIYVFEAEVLTGSFCQGNSSNIIPPPLSPGALDVNDSVVDNVSSPETIVVFNGMQAMP
LYLWTCTQDRTFSQHPMWSQDYSSGPGMVSSLQSWEWVLNGSSV

Fig. 2 (continued)

Fig. 3

610015	480 ENGLEARSPAIN		500 TEAHAWIQRI	LSLQNHHIIE	520 NNHILYLGRK	
-	RGGLEAGSPAII 480					
610015	540 KTSSVSITEII:	: . :::.:		: :: ::: :	:::::	.:: ::
-	TSTRVSISETVS 540	SPRTATLEIKO 550	SPQADLIDAV 560	MRIECMLCDV 570	QEEVAGKREK 580	NLWSLSGQG 590
610015	600 TIQQQKTQDEM	610 KENIIFLKCPV	620 PPTQELLDQ	630 KKQFEKCGLQ	640 VLKVEKIDNE	650 VLMAAFQRK
-	TNQQEKL-DKM 600					
610015	660 KKMMEEKLHRQ			VGFQRMYSTP		
-	KKMMEERTPKG	SGSQRLFQQVI 670	PHQFCNTVCR 680	VGFHRMYSTS 690	YNPVYGAGIY 700	
610015	720 EKAKKISAADK	730 LIYVFEAEVLT	740 IGFFCQGHPL	750 NIVPPPLSPG	760 AIDGHDSVVD	770 NVSSPETFV
_	DKVKKTSSTDK 720	:::::::::		::.:::::	::: ::::::	::::::::
610015	780 IFSGMQAIPQY					PVD
_	VFNGMQAMPLY	LWTCTQDRTF		:::: SSGPGMVSSL 810	. : :: .QSWEWVLNGS 820	: SV-

Fig. 3 (continued)

3244n 3024n

Comparison of: (A) 7486572155.52.67.361 >_ BAL Human (B) 7486572155.52.67.362 >_ BAL Mouse using matrix file: DNA, gap penalties: -16/-4								
71.	7% identity	in 2916 r	t overlap;	score: 544	4			
<u>-</u>	::: ::	: ::: :	TGGTGCTCTTG	GAGAAAACTA	TAGTTGGCAA	:::::::		
_	430 AACCACAATG	440 ACTTCAAAAT	450 'TTTAAAAAATA		<del>-</del> · ·	480 GTCCTCCAG		
	AAACACAATG 260		::::::::::::::::::::::::::::::::::::::	::::: :::: ATGAGAGTCA 290		::::::: GTCCTCCAA 310		
_			510 TACCCTGGTCT	CTCCAGTTCA	GGAAGGCAAC			
	AATAAGTTTG 320	GATGCATCTO 330	TACCCTGAGCT 340	GTCCAACTCT. 350	AGCAGGGAGC 360	AGCTCTCCT 370		
_	:: ::	: :::::::	570 AATGCTGACTC : :::: : GACCCTGATCC	:: ::::::	::::::	:::::		
-	380	390	400	410	420	430		
_			630 TGATGCTGTGG		650 CAATGAAGAT(	660 CTTCTGCAT		
_			TGATGCTGTGG 460			CTTTTGCAT 490		
_	:: ::::	:::::	CCTGGTAAAAG	:::::::	TGAAATCCAA(	::::::::		
_	GGAAGTGGCC 500	TGGCCGGAAC 510	CTTGGTGAAAA 520	CTGGTGGCTT 530	TGAAATCCAA 540	GAAGAGAGC 550		
_	::: :	:::::	750 ATGGTAAAGTGT ::::::::::::::::::::::::::	::: :::::	:: ::: ::	:: :: ::		
	560	570	580	590	600	610		

Fig. 4 SUBSTITUTE SHEET (RULE 26)

Light to the

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Fig. 4 (continued)

	1050	1260	1270	1200	1200	1200
	1250	1260 സസമാദ്യവസ്തവ		1280 ************************************		1300 CAGGAGTTGAAATG
_	:: :::			HANGICANII		DIARADII DADUA.
						AGGGGTTGAAATG
-	11			120 11		40 1150
	1310	1320	1330	1340	1350	1360
		AATTTCTTG(				GTTGGTACTGGTC
	:: ::	:: ::::	:: :::	::: : ::	: :::	
_	GAAAAGG	AACTTG!	ACAAGGT			AGAGGTGTGGGTC
	11	60	1170	1180	1190	1200
	1370	1380	1390			1420
_						GCATTCAGAATTT
						GCATTCCCAAATC
_	1210	1220	1230	TATGTCTTCC	ATGTGGCATG	1260
	1210	1220	1230	1240	1250	1200
	1430	1440	1450	1460	1470	1480
						ATGCATTGAGCAA
_	:::				<del></del>	
	AACAAAT					ATGCCTTAAACCA
_	1270	1280	1290	1300	1310	1320
	1490	1500	1510			1540
_						AATAAAGAAGGAA
	1330	1340	1350	TCTCGGGACAC	GATTGATGGA 1370	TTTGAAGAAGAGT 1380
	1330	1340	1330	1300	1370	1300
	1550	1560	1570	1580	1590	1600
						CCATGTAAAACAC
_	::::::	: ::::	:::::::			:: :::
_	ACAGCAG	CTCAGATAAT			TTTGCTAAAGA	GCACAAGGAAAAA
	1390	1400	1410	1420	1430	1440
		4.400	4.000	4 4 4 4		4.444
	1610		1630			1660
_					PTGGAGATATA	TAAGGCTTTCAGT
						CAAGATTTTTAT
-	1450	1460	1470	1480	1490	1500
	1430	1400	1470	1400	1430	1300
	1670	1680	1690	1700	1710	
_				GCTGAGTTTG	AACAATTACAG	STGTC
		:: :::: ::		::::: : :		
_						STGGTGCTTTAGCC
	1510	1520	1530	1540	1550	1560

Fig. 4 (continued)

	1720	1730	1740	1	.750	1760	1770	
_	CCCCAG	TCAACCAG.	AGAGGAG:			GCTTGAAGC		TGCCATC
	: :::		: ::::		: ::			::::::
_						CCTTGAAGC		
	1570	158	0	1590	1600	161	0 16	20
	1780	1790	1800	1	.810	1820	1830	
						AGGCCCACG		ייי א מב <i>ו</i>
_	:::::		:: ::::			::::::::		iiii :
_	AATCTC	ATGGGTGT	AAAAGTG(		TGT-GTG	AGGCCCAGG	AATGGATTG	
	1630	164		L650	1660			680
	1040	4000	4060	_				
	1840				870		1890	
_	CCTGAG				GAGAATA	ATCATATTC'		GGAGAAA
						ATCATATTC'	· ∶∶∶∶∶∶∶ ԻՐͲΣͲՐͲͲԸ	CCAAAAA
_	1690	17(		1710	1720			740
				_			-	
	1900	1910			930		1950	
_						CAAGTGTCT		AAATTAT
_	1750	176	IGICIGAC So	1770	ACCAGCAC 1780	CAAGAGTCT() 179		AGACTGT 800
	±1,00	<b>±</b> /\	, ,	1///	1/00	, 1/3	7U 1	000
							_	
	1960	1970			990	2000	2010	
_			CAGAGTTA	GAGATT	GAAGGAG		2010	AGGTGGT
_	CAGCCCA	GGAAGGA	CAGAGTTA	GAGATT	GAAGGAGG	2000 CCGGGCTG	2010 ACCTCATTG	: : ::
<del>-</del>	CAGCCCA ::::::: CAGTCCA	AGGAAGGA( AGAACGG(	CAGAGTTA : :: CACTTTG	GAGATT ::::: GAGATT	GAAGGAGC :::: AAAGGTCC	2000 CCGGGCTGA	2010 ACCTCATTG	: : :: ACGCAGT
<u>-</u>	CAGCCCA	GGAAGGA	CAGAGTTA : :: CACTTTG	GAGATT	GAAGGAGC :::: AAAGGTCC	2000 CCGGGCTGA	2010 ACCTCATTG	: : ::
<b>-</b>	CAGCCCA ::::::: CAGTCCA	AGGAAGGA( AGAACGG(	CAGAGTTA : :: CCACTTTG	GAGATT GAGATT 1830	GAAGGAGO ::::: AAAGGTCO 1840	2000 CCCGGGCTGI CCCAGGCTGI	2010 ACCTCATTG CCTCATTG ACCTCATTG	: : :: ACGCAGT
-	CAGCCCA ::::::: CAGTCCA 1810	AGGAAGGAC ::::::::::::::::::::::::::::::	CAGAGTTA : :: CCACTTTG 2040	GAGATT ::::: GAGATT 1830	GAAGGAGO :::::::::::::::::::::::::::::::	2000 CCCGGGCTGA CCCAGGCTGA 185	2010 ACCTCATTG SILLILIA ACCTCATTG 50 18	: : :: ACGCAGT 860
_	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC :::::	AGGAAGGA( LAGAACGG( 182 2030 LATTGAAGA	CAGAGTTA  CCACTTTG  O  2040  ATATGCTT  ::::::	GAGATTO	GAAGGAGO ::::  AAAGGTCO 1840 050 GTACAGGA	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC	2010 ACCTCATTG ACCTCATTG 50 18 2070 AAAGGAAAA	: : :: ACGCAGT 860 AGGAGCG
- - -	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG	AGGAAGGAC LAGAACGGC 182 2030 LATTGAAGA LIIIII	CAGAGTTA CCACTTTG O 2040 ATATGCTT CTATGCTG	GAGATTO	GAAGGAGO ::::: AAAGGTCO 1840 050 GTACAGGA :::::::	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC LAGAAGTGGC	2010 ACCTCATTG ACCTCATTG 50 18 2070 AAAGGAAAA : : : : : : :	E : :: ACGCAGT 860 AGGAGCG :::: GGGAGAA
-	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC :::::	AGGAAGGA( LAGAACGG( 182 2030 LATTGAAGA	CAGAGTTA CCACTTTG O 2040 ATATGCTT CTATGCTG	GAGATTO	GAAGGAGO ::::  AAAGGTCO 1840 050 GTACAGGA	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC LAGAAGTGGC	2010 ACCTCATTG ACCTCATTG 50 18 2070 AAAGGAAAA : : : : : : :	: : :: ACGCAGT 860 AGGAGCG
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870	AGGAAGGAC  LAGAACGGC  182  2030  CATTGAAGA  LLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	CAGAGTTA CCACTTTG 2040 ATATGCTT CTATGCTG	GAGATTO	GAAGGAGC :::::::::::::::::::::::::::::::	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC :::::::	2010 ACCTCATTG SCCTCATTG SO 18 2070 CAAGGAAAA : : : : : : : : : : : : : : : : : :	E : :: ACGCAGT 860 AGGAGCG :::: GGGAGAA
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870	AGGAAGGAC  182  2030  ATTGAAGA  ::::::  ATTGAAGA  2090	CAGAGTTA CACTTTG CO CACTTTG CO CATATGCTTG CO CATATGCTG CO CATATGCT C	GAGATTO SERVICE SERVIC	GAAGGAGC :::::::::::::::::::::::::::::::	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC ::::::: AGAAGTGGC 191	2010 ACCTCATTG SCCTCATTG 50 18 2070 CAAGGAAAA : : : : : : : : : : : : : : : : : :	E : :: ACGCAGT B60  AGGAGCG :::: GGGAGAA
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870	AGGAAGGAC LICEL SEAGAACGGC LATTGAAGA LICEL SEATTGAATG LATTGAATG	CAGAGTTA CACTTTG CO CACTTTG CO CATATGCTTG CO CATATGCTG CO CATATGCT CO	GAGATT  CAGAGATT  AND CAGAGATT  AND CAGAGATT  AND CAGAGATT  AND CAGAGATT  CAGAGATT  CAGAGATT  CAGAGATT  CAGAGATT  CAGAGATT  CAGAGATT  CAGAGATT  CAGAGATT  CAGAGAT  CA	GAAGGAGC :::: AAAGGTCC 1840 050 GTACAGGA :::::: GTTCAGGA 1900 110 ACTATTCA	2000 CCCGGGCTGA CCCAGGCTGA 2060 AGGAAATGGC ::::::: AGAAGTGGC 191 2120 AGCAACAAAA	2010 ACCTCATTG SCCTCATTG 50 18 2070 AAAGGAAAA : : : : : : AGGAAAAA 0 19 2130 AAACCCAAGA	ACGAAAT
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870  2080 AGGCCTT :::::	AGGAAGGAC  AGGAACGGC  182  2030  ATTGAAGA  :::::::  ATTGAATC  188  2090  TGGCGCTC	CAGAGTTA CACTTTG CO CATATGCTT CACTTTGCTG CATATGCTG CATAT	GAGATT  CAGAGATT  GAGATT  1830  TGTAAA  CCAGTGAC  CAGTGG  CCAGTGG  CCAGTG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGC  CCAGTGG  CCAGTGC  CCAGTGG  CCAGTGC  CCAGTGC  CCAGTGC  CCAGTG  CCAGTGC  CCAGTC  CCAGTGC  CCAGTGC  CCAGTGC  CCAGTGC  CC	GAAGGAGG :::: AAAGGTCC 1840 050 GTACAGGA :::::: GTTCAGGA 1900 110 ACTATTCA	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC ::::::: AGAAGTGGC 191	2010 ACCTCATTG CCTCATTG 50 18 2070 AAGGAAAAA CO 19 2130 AACCCAAG	ACGCAGT  AGGAGCG  SGGAGAA  ACGAAAT
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870  2080 AGGCCTT :::::	AGGAAGGAC  AGGAACGGC  182  2030  ATTGAAGA  :::::::  ATTGAATC  188  2090  TGGCGCTC	CAGAGTTA CAGAGTTA CAGAGTTA CAGAGTTA CAGAGTTA CAGAGTTA CAGAGTTA CAGAGTTA CAGAGGTTA CAGA	GAGATT  CAGAGATT  GAGATT  1830  TGTAAA  CCAGTGAC  CAGTGG  CCAGTGG  CCAGTG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGG  CCAGTGC  CCAGTGG  CCAGTGC  CCAGTGG  CCAGTGC  CCAGTGC  CCAGTGC  CCAGTG  CCAGTGC  CCAGTC  CCAGTGC  CCAGTGC  CCAGTGC  CCAGTGC  CC	GAAGGAGG :::: AAAGGTCC 1840 050 GTACAGGA :::::: GTTCAGGA 1900 110 ACTATTCA	2000 CCCGGGCTGA CCCAGGCTGA 2060 AGGAAATGGC 191 2120 AGCAACAAAA	2010 ACCTCATTG ACCTCATTG ACCTCATTG ACCTCATTG AAAGGAAAAA AAAGGAAAAAA AAAAAAAAAA	ACGCAGT  AGGAGCG  SGGAGAA  ACGAAAT
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870  2080 AGGCCTT ::::: AAATCTT 1930	AGGAAGGAC  182  2030  ATTGAAGA  ::::::  ATTGAATC  188  2090  TGGCGCTC  ::::::  TGGAGCTT  194	CAGAGTTA CONTROL CONTR	GAGATTO CONTROL CONTRO	GAAGGAGC :::::::::::::::::::::::::::::::	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC 191 2120 AGCAACAAAA CCCAAGAAAAA 197	2010 ACCTCATTG CCTCATTG COTCATTG CAAGGAAAA CCTCATTG CAAGGAAAAA CCTCATGA CAAGGAAAAA CCCAAGA CCCAAGA CCCAAGA CCCAAGA CCCAAGA CCCAAGA CCCAAGA CCCAAGA CCCAAGA	ACGAAAT  COAAAAT  COAAAAT
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870  2080 AGGCCTT ::::: AAATCTT 1930	AGGAAGGAC  182  2030  ATTGAAGA  ::::::  ATTGAATC  188  2090  TGGCGCTC  ::::::  TGGAGCTT  194	CAGAGTTA  CACTTTO  2040  ATATGCTT  CACTTAGCTO  2100  CGTTAGGA  CGTTAGGA  CGTCAGGA  CGTCAGGA  CGTCAGGA  CGTCAGGA  CGTCAGGA  CGTCAGGA  CGTCAGGA  CGTCAGGA	GAGATTI SGAGATTI 1830  TGTAAA TGTGAC 1890  CAGTGGI CAGGGGGI 1950	GAAGGAGG ::::::::::::::::::::::::::::::	2000 CCCGGGCTGA CCCAGGCTGA 185 2060 AGGAAATGGC 191 2120 AGCAACAAAA 1197 2180	2010 ACCTCATTG S:::::::: ACCTCATTG 50 15 2070 AAAGGAAAAA ::::::: AGGAAAAAA .0 15 2130 AAACCCAAGA ::::::: AACTGGA	ACGAAAT  ACGAAAT  ACGAAAT  ACGAAAT  1980
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870  2080 AGGCCTT :::: AAATCTT 1930  2140 GAAAGAA	AGGAAGGAC  182  2030  ATTGAAGA  ::::::  ATTGAATC  188  2090  TGGCGCTC  ::::::  TGGAGCTT  194  2150  AATATCAT	CAGAGTTA  CACTTTG  2040  ATATGCTG  CATATGCTG  2100  CGTTAGGA  CGTCAGGA	GAGATT  CAGAGATT  1830  TGTAAA  CCAGTGAC  CAGTGGC  CCAGTGGC  CCAGTGCC  CCAGTGGC  CCAGTGCC  CCAGTGGC  CCAGTGCC  CCAGTCC  CCAGTGCC  CCAGTGCC  CCAGTCC  CCAGTC  CCAGTCC  C	GAAGGAGG  :::::  AAAGGTCC  1840  050  GTACAGGA  :::::::  GTTCAGGA  1900  110  ACTATTCA  1960  170  CCTGTGCC	2000 CCCGGGCTGA CCCAGGCTGA 2060 AGGAAATGGC AGGAAATGGC 191 2120 AGCAACAAAA CCCAACAAAA 197 2180 CTCCAACTCA	2010 ACCTCATTG CCTCATTG COTTCATTG CO	ACGAAAT  ACGAAAT  ACGAAAT  ACGAAAT  1980
	CAGCCCA ::::::: CAGTCCA 1810  2020 TATGAAC ::::: TATGAGG 1870  2080 AGGCCTT ::::: AAATCTT 1930  2140 GAAAGAA ::::::	AGGAAGGAC  182  2030  ATTGAAGA  ::::::  ATTGAATC  188  2090  TGGCGCTC  ::::::  TGGAGCTT  194  2150  AATATCAT	CAGAGTTA  CACTTTG  COACTTTG  COACTTT	GAGATT  CHARACTER  CAGTGAC  CAGTGGC  CAGGGGC  CAGGGCC  CAGGGGC  CAGGGCC  CAGGCC  CAGCC  CAGGCC  CAGCC  CAGGCC  CAGCC  CACCC  CACCC  CACCC  CACCC  CACC  CACCC  CACC  CACCC	GAAGGAGG  :::::  AAAGGTCC  1840  050  GTACAGGA  :::::::  GTTCAGGA  1900  110  ACTATTCA  ::::::  ACCAACCA  1960  170  CCTGTGCCC:::::::	2000 CCCGGGCTGA CCCAGGCTGA 2060 AGGAAATGGC AGGAAATGGC 191 2120 AGCAACAAAA CCCAACAAAA 197 2180 CTCCAACTCA	2010 ACCTCATTG COTTCATTG C	ACGCAGT B60 AGGAGCG :::: GGGAGAA B20 ACGAAAT ::::: ATAAAAT 1980 FAGATCA

Fig. 4 (continued)

	2200 AAAGAA	2210 ACAGTTTG	2220 AAAAATGTGG	2230 TTTGCAGGTT	2240 CTAAAGGTGG	2250 SAGAAGATAGA	САЗТСЗ
_	:::::	::::::::	:::: :::::	::: ::::			
_				CTTGTGGGTT			
	2	050	2060	2070	2080	2090	2100
	2260	2270	2280	2290	2300	2310	
_				AAAGAAGAAA			CAGGCA
_	::: ::	::::::	:::: :::	* * * * * * * * * * *	* * * * * * * * * * * * * * * * * * * *	:: ::	: :
_				GAAGAAGAAA			
	2	110	2120	2130	2140	2150	2160
	2320	2330	2340	2350	2360	2370	
_		GAGCCATA		GCAAGTCCCA			ATGCAG
				• • • • • • • • • • • • • • • • • • • •		:::::	:::::
_				GCAGGTCCCA			
	4.	170	2180	2190	2200	2210	2220
	2380	2390	2400	2410	2420	2430	
_	AGTTGG	CTTTCAAAG		GACACCTTGC			CATATA
	::: ::	::: :: ::		:::: : :			:::::
_	AGTCGG	CTTCCACAG		GACATCCTAT			
		מככ					
	2:	230	2240	2250	2260	2270	2280
	2440	230 2 <b>4</b> 50	22 <b>4</b> 0 2 <b>4</b> 60	2470	2480	2490	2280
_	2440	2450	2460		2480	2490	
_	2440 CTTCACO	2450 CAAGAACCI	2460 CAAAAACCT(	2470 GGCAGAGAAG	2480 GCCAAGAAAA	2490 TCTCTGCTGC	AGATAA
_ _	2440 CTTCACC ::::: TTTCACC	2450 CAAGAACCT	2460 CAAAAACCT(	2470 GGCAGAGAAG ::::::::	2480 GCCAAGAAAA : ::::::: GTCAAGAAAA	2490 TCTCTGCTGC ::: :	AGATAA ::::::
_ _	2440 CTTCACC ::::: TTTCACC	2450 CAAGAACCI	2460 CAAAAACCT(	2470 GGCAGAGAAG	2480 GCCAAGAAAA	2490 TCTCTGCTGC	AGATAA
_	2440 CTTCACO :::::: TTTCACO 22	2450 CAAGAACCT ::::::::: CAAGAGCCT 290 2510	2460 CCAAAAACCT( ::::::::::: CCAAAAATCTI 2300 2520	2470 GGCAGAGAAG ::::: ::: AGCAGACAAG 2310 2530	2480 GCCAAGAAAA : ::::::: GTCAAGAAAA 2320 2540	2490 TCTCTGCTGC ::: : CCTCAAGCAC 2330	AGATAA ::: :: AGACAA 2340
_	2440 CTTCACO :::::: TTTCACO 22	2450 CAAGAACCT ::::::::: CAAGAGCCT 290 2510	2460 CAAAAACCT( :::::::::::::::::::::::::::::::::::	2470 GGCAGAGAAG :::::::::: AGCAGACAAG 2310 2530 AGTACTCACA	2480 GCCAAGAAAA : ::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT	2490 TCTCTGCTGC ::: : CCTCAAGCAC 2330	AGATAA ::: :: AGACAA 2340
- -	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC	2450 CAAGAACCT CAAGAGCCT 290 2510 CTATGTGTT	2460 CAAAAACCTO CCAAAAATCTO 2300 2520 TGAGGCTGAA	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT :::::::	2490 TCTCTGCTGC ::: : CCTCAAGCAC 2330  2550 GCCAGGGACA	AGATAA :::::: AGACAA 2340 TCCGTT
- - -	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC ::::::: GCTAATC	2450 CAAGAACCT CAAGAGCCT 290 2510 CTATGTGTT CTATGTGTT	2460 CAAAAACCTO CCAAAAATCTO 2300 2520 TGAGGCTGAA	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : ::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT :::::::	2490 TCTCTGCTGC ::: : CCTCAAGCAC 2330  2550 GCCAGGGACA : :::: : GTCAGGGTAA	AGATAA :::::: AGACAA 2340 TCCGTT :::: TTCCTC
- -	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC ::::::: GCTAATC	2450 CAAGAACCT CAAGAGCCT 290 2510 CTATGTGTT CTATGTGTT	2460 CAAAAACCTO CCAAAAATCTO 2300 2520 TGAGGCTGAA	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT :::::::	2490 TCTCTGCTGC ::: : CCTCAAGCAC 2330  2550 GCCAGGGACA	AGATAA :::::: AGACAA 2340 TCCGTT
	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC ::::::: GCTAATC 23	2450 CAAGAACCT CAAGAGCCT 290 2510 CTATGTGTT 350 2570	2460 CCAAAAACCTC CCAAAAATCTZ 2300 2520 TGAGGCTGAZ CTGAGGCAGAZ 2360 2580	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT :: ::::: GGGTCCTTCT 2380 2600	2490 TCTCTGCTGC ::: : CCTCAAGCAC 2330 2550 GCCAGGGACA ::::: : GTCAGGGTAA 2390 2610	AGATAA :::::: AGACAA 2340 TCCGTT :::: TTCCTC 2400
- -	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC ::::::: GCTAATC 23	2450 CAAGAACCT CAAGAGCCT 290 2510 CTATGTGTT CTATGTGTT 350 2570 CGTTCCCCC	2460 CAAAAACCTC CCAAAAATCTZ 2300 2520 TGAGGCTGAZ CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT ::::::: GGGTCCTTCT 2380 2600 ATAGATGGTC	2490 TCTCTGCTGC ::: : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : GTCAGGGTAA 2390  2610 ATGACAGTGT	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA
	2440 CTTCACC ::::: TTTCACC 22 2500 GCTGATC :::::: GCTAATC 23 2560 AAATATT	2450 CAAGAACCT CAAGAACCT 290 2510 CTATGTGTT CTATGTGTT 350 2570 CGTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2460 CAAAAACCTC CCAAAAATCTZ 2300 2520 TGAGGCTGAZ CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT ::::::: GGGTCCTTCT 2380 2600 ATAGATGGTC	2490 TCTCTGCTGC ::: : : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : GTCAGGGTAA 2390  2610 ATGACAGTGT ::::: :	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA
- - -	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC :::::: GCTAATC 23 2560 AAATATT :::::: AAATATC	2450 CAAGAACCT CAAGAGCCT 290 2510 CTATGTGTT 350 2570 PGTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2460 CAAAAACCTC CCAAAAATCTZ 2300 2520 TGAGGCTGAZ CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAAA 2320 2540 GGCTTCTTCT :::::::: GGGTCCTTCT 2380 2600 ATAGATGGTC :::::: TTAGATGTCA	2490 TCTCTGCTGC ::: : : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : GTCAGGGTAA 2390  2610 ATGACAGTGT ::::: : ATGACAGCGT	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA :::: AGTTGA
	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC :::::: GCTAATC 23 2560 AAATATC :::::: AAATATC	2450 CAAGAACCT CAAGAGCCT 290 2510 CTATGTGTT CTATGTGTT 350 2570 CGTTCCCCCCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	2460 CCAAAAACCTO CCAAAAACCTO CCAAAAATCTO 2300 2520 TGAGGCTGAO CTGAGGCAGAO 2360 2580 CACCACTGAGT CACCAC	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT ::::::: GGGTCCTTCT 2380 2600 ATAGATGGTC	2490 TCTCTGCTGC ::: : : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : GTCAGGGTAA 2390  2610 ATGACAGTGT ::::: :	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA
- - -	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC :::::: GCTAATC 23 2560 AAATATC :::::: AAATATC 24	2450 CAAGAACCT CAAGAACCT 290 2510 CTATGTGTT 350 2570 CGTTCCCCC CATCCCTCC	2460 CCAAAAACCTO CCAAAAATCTA 2300  2520 TGAGGCTGAA CCACTGAGAA 2360  2580 CACCACTGAGAA CACCACTGAGAA 2420  2640	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT :: ::::: GGGTCCTTCT 2380 2600 ATAGATGGTC :::::: TTAGATGTCA 2440 2660	2490 TCTCTGCTGC ::: : : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : GTCAGGGTAA 2390  2610 ATGACAGTGT ::::: :: ATGACAGCGT 2450	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA ::::: AGTTGA 2460
	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC :::::: GCTAATC 23 2560 AAATATC ::::: AAATATC 24 2620 CAATGTC	2450 CAAGAACCT CAAGAACCT 290 2510 CTATGTGTT 350 2570 PGTTCCCCC CATCCCTCC	2460 CCAAAAACCTC :::::::::::::::::::::::::::	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : :::::::: GTCAAGAAAA 2320 2540 GGCTTCTTCT :: ::::: GGGTCCTTCT 2380 2600 ATAGATGGTC :::::: TTAGATGTCA 2440 2660 AGTGGCATGC	2490 TCTCTGCTGC ::: : : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : GTCAGGGTAA 2390  2610 ATGACAGTGT ::::: :: ATGACAGCGT 2450  2670 AGGCTATACC	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA ::::: AGTTGA 2460
	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC :::::: GCTAATC 23 2560 AAATATC 24 2620 CAATGTC ::::::	2450 CAAGAACCT CAAGAACCT 290  2510 CTATGTGTT 350  2570 CGTTCCCCC CATCCCTCC 410  2630 CTCCAGCCC	2460 CCAAAAACCTC CCAAAAACCTC CCAAAAATCTC 2300  2520 TGAGGCTGAC CTGAGGCAGAC 2360  2580 ACCACTGAGC CACCACTGAGC CACCACTGAGCACTGAGC CACCACTGAGCACTACTCACTGAGC CACCACTGAGCACTACTACTACTACTACTACTACTACTACTACTACTACT	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : ::::::::::::::::::::::::::::::	2490 TCTCTGCTGC ::: : : : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : : GTCAGGGTAA 2390  2610 ATGACAGTGT ::::: : :: ATGACAGCGT 2450  2670 AGGCTATACC :::: : : :	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA ::::: AGTTGA 2460  TCAGTA
	2440 CTTCACC :::::: TTTCACC 22 2500 GCTGATC :::::: GCTAATC 23 2560 AAATATC ::::: AAATATC 24 2620 CAATGTC :::::: CAATGTC	2450 CAAGAACCT CAAGAACCT 290  2510 CTATGTGTT 350  2570 CGTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2460 CCAAAAACCTC CCAAAAACCTC CCAAAAATCTC 2300  2520 TGAGGCTGAC CTGAGGCAGAC 2360  2580 ACCACTGAGC CACCACTGAGC CACCACTGAGCACTGAGC CACCACTGAGCACTACTCACTGAGC CACCACTGAGCACTACTACTACTACTACTACTACTACTACTACTACTACT	2470 GGCAGAGAAG ::::::::::::::::::::::::::::	2480 GCCAAGAAAA : ::::::::::::::::::::::::::::::	2490 TCTCTGCTGC ::: : : : CCTCAAGCAC 2330  2550 GCCAGGGACA ::::: : : GTCAGGGTAA 2390  2610 ATGACAGTGT ::::: : :: ATGACAGCGT 2450  2670 AGGCTATACC :::: : : :	AGATAA :::::: AGACAA 2340  TCCGTT :::: TTCCTC 2400  GGTTGA ::::: AGTTGA 2460  TCAGTA

Fig. 4 (continued)

TTTGTGGACATGCACCCAGGAATATGTACA			690 2			2710	
CTTGTGGACTTGCACACAGGATAGGACATTCTCACAGCATCCGATGTGGTCACAGGACTA 2530 2540 2550 2560 2570 2580  2730 2740 2750 2760 2770 2780  CTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGGCAG ::::::::::::::::::::::::::::::::::	_						
2530 2540 2550 2560 2570 2580  2730 2740 2750 2760 2770 2780  CTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGGCAG  CTCATCAGGACCAGGAATGGTCTCTTCGCTGCAGTCCTGGGAATGGGTCTTAAATGGCAG		:::::::	: ::::: ::		: ::		
2730 2740 2750 2760 2770 2780  CTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGGCAG  CTCATCAGGACCAGGAATGGTCTCTTCGCTGCAGTCCTGGGAATGGGTCTTAAATGGCAG	_		CTTGCACACA	GGATAGGACA	TTCTCACAGCA	TCCGATGTGG	
CTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGGCAG ::::::::::::::::::::::::::::::::::		253	0 254	0 255	0 2560	2570	2580
CTCATCAGGACCAATGAGACCCTTTGCACAGCATCCTTGGAGGGGATTCGCAAGTGGCAG ::::::::::::::::::::::::::::::::::		272	. 274	0 275	0750	0550	0700
CTCATCAGGACCAGGAATGGTCTCTTCGCTGCAGTCCTGGGAATGGGTCTTAAATGGCAG							
CTCATCAGGACCAGGAATGGTCTCTCGCTGCAGTCCTGGGAATGGGTCTTAAATGGCAG							
		CMCAMCAC	:::::: :::::::::::::::::::::::::::::::		: ::: : ::	: ::	
2590 2000 2010 2020 2030 2040							
		233	200	0 201	2020	2030	2040
2790 2800 2810 2820 2830 2840		279	0 280	0 281	า วยวก	2020	2040
CCCTGTTGATTAATCTCTACATCATTTTAACAGCTGGTATGGCCTTACCTTGGGTGAACT							
_ ::::: ::::::::::::::::::::::::::::::	-						
_ CTCTGTTTAGTGTCTACATCAGTTTAACAAGCAGAAGGGGTTGAGAGAACT					AACAAGCAGAA		
2650 2660 2670 2680 2690	_						
2030					<b>.</b>		2050
2850 2860 2870 2880 2890 2900		285	0 286	0 287	2880	2890	2900
AACCAAATAATGACCATCGATGGCTCAAAGAGTGGCTTGAATATATCCCATGGGTTATCT							
	_						
GACAAAATGATAAATAACAGGTTACCT	_	GACAAAAT	GAT	<b>-</b> AA	TA	A	CAGGTTACCT
2700 2710		2700					
· ·			`				
2910 2920 2930 2940 2950 2960			0 292	0 2930	2940	2950	2960
GTATGGACTGACTGGGTTATTGAAAGGACTAGCCACATACTAGCATCTTAGTGCCTTTAT	_						
:: ::::::::::::::::::::::::::::::::::::							
GTTCAGAATGATGGGGTCACTAAAGGCACCACACACACAC	_	GTTCAGAA'	TGATGGGGTC.	ACTAAAGGCA(	CGACCACACA	CTAGCATCATA	
2720 2730 2740 2750 2760 2770		2720 2	730 2	740 27	750 27	60	0
2070 2000 2000 2000 2000		207	0 000		2000	224	
2970 2980 2990 3000 3010 3020							
_ CTGTCTTATGTCTTGGGGTTGGGGTAGGTAGATACCAAATGAAACACTTTCAGGACCTT	-						
GTCTTTACCTCTGGGCTTGACTGGGCAGATGCCAGCTAAAACTTCCTCACTGT							
2780 2790 2800 2810 2820 2830	-	2780	2790	2800 2800	2010		
2700 2750 2000 2010 2020 2030		2700	2130	2000	2010	2020	2030
3030 3040 3050 3060 3070		3030	0 304	3050	3060		3070
_ CCTTCCTCTTGCAGTTGTTCTTTAATCTCCTTTACTAGAGGAGATAAATATTTTG							
	_						
CTTTTCTATTTGACATCTTTCATCTCCTTTCCTATAGGTGACAGCAAGAATACTTTA		CTTTTCTA	TTTGACA'	PCTTTCATCT(	CTTTCCTATA	GGTGACAGCAA	GAATACTTTA
2840 2850 2860 2870 2880	_						

Fig. 4 (continued)

PCT/US99/25439

	3080	3090	3100	3110	3120	3130	
_	CATATAA	TGAAGAAAT?	TTTTCTAGTA:	rataacgcagg(	CCTTTTATTT	TCTAAAATGAT(	ξA
	::: ::	: :: :::	:::::	:: ::	•••••••	:::::::::	
_	TATAGAA	CAAGGATATI	TTTTT	CAAG(	CTGTTATTT	TCTAAAATGA	
	2890	2900		2910	2920	2930	
	3140	3150	3160	3170	3180	3190	
_	TAGTATA	<b>AAAATGTTA</b> (	GATAACAGAI	ATGATTTTAGAT	TTTCCAGAG	AATATTATAAAG	T
	***	:: :::	::: ::::: :	******* ** *	:::::::::::::::::::::::::::::::::::::::	::: ::::::::	:
_	TAGCACA	AACTAG	GACAACAGG	<b>TGATTTCAGG</b>	TTTCTATAT	AAT-TTATAAAG	T
	2940		2950	2960 2	970	2980	
	3200	3210	3220	3230			
	GCTTTAG	GTATGAAAAT	AAATCATCTT	TGTCTGATT		-	
_		• • • • • • •					
	CCMMMCC	 חגגגממחגחה	AAATCACCTT	IMCIMCIMCA CM			
_							
	2990	3000	3010	3020			

Fig. 4 (continued)

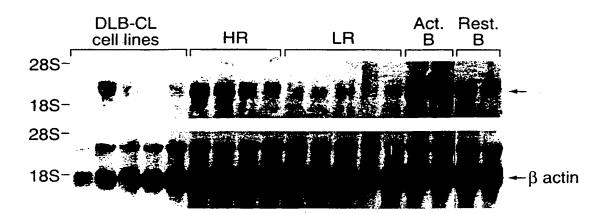
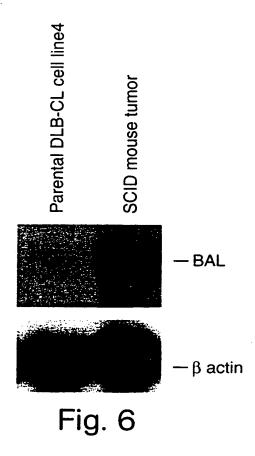
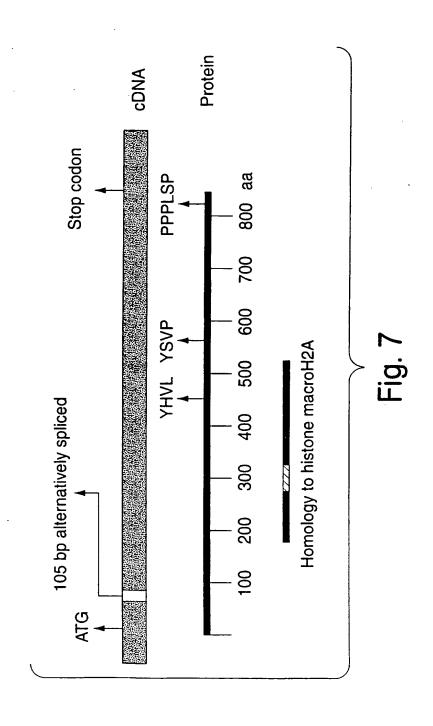


Fig. 5





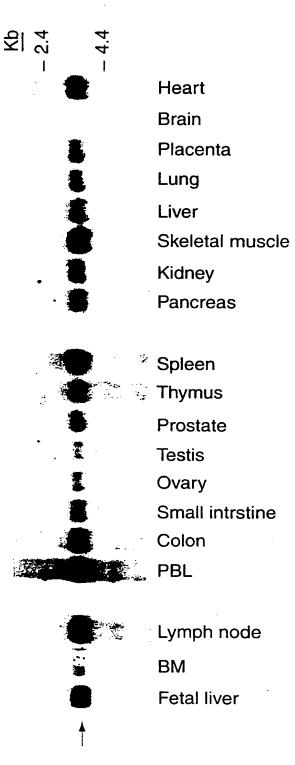


Fig. 8

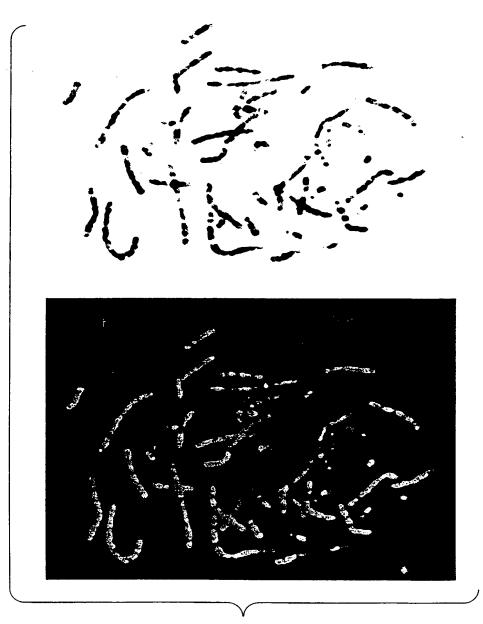


Fig. 9

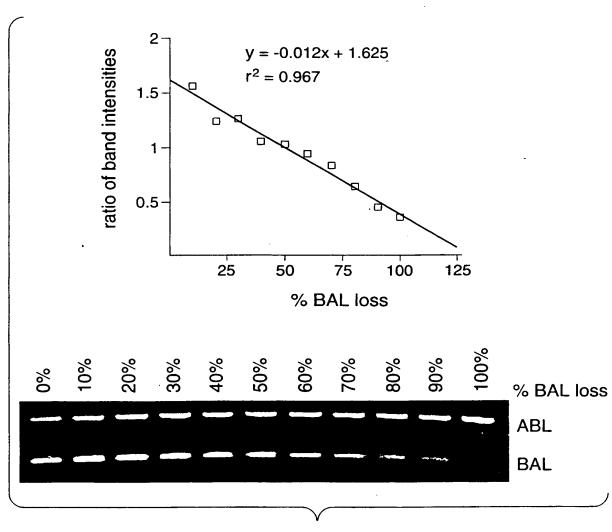
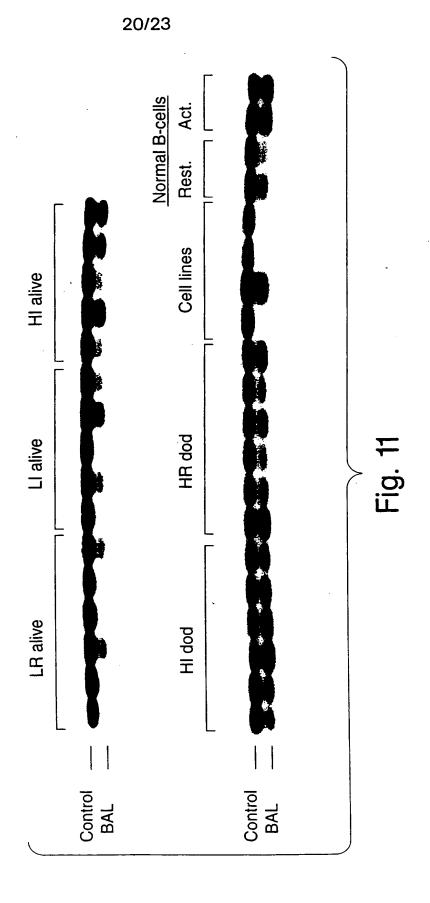


Fig. 10



**SUBSTITUTE SHEET (RULE 26)** 

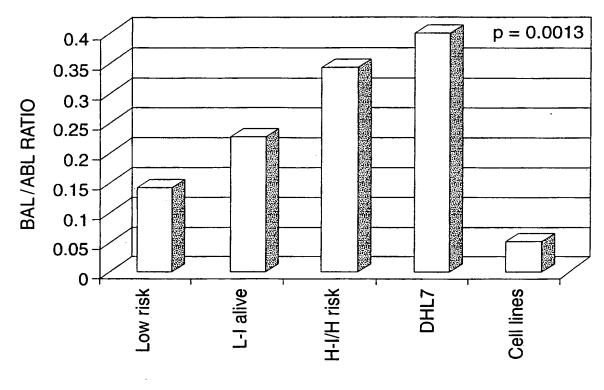


Fig. 12

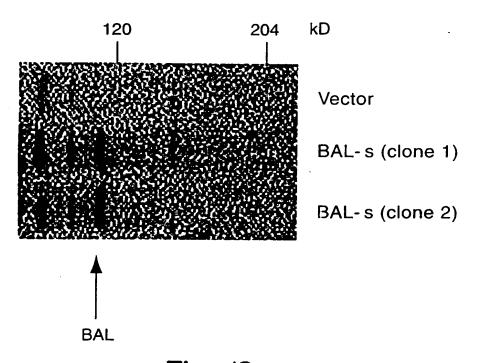


Fig. 13

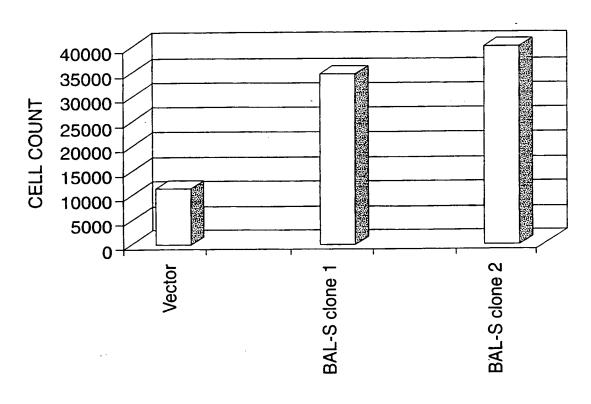


Fig. 14